



#8

EXPRESS MAIL NO. EL755728058US

SEQUENCE LISTING

<110> White, Aaron P.
Doran, James L.
Collinson, S. Karen
Kay, William W.

<120> BACTERIAL FIMBRIAL SYSTEM FOR
PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

<130> 920043.406

<140> US 09/543,407

<141> 2000-04-05

<160> 59

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 456

<212> DNA

<213> Salmonella enteritidis

<400> 1

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ggcgctcggtt cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc	120
ccggactcaa cggtgagcat ttatcagtac gggtccgcta acgctgcgct tgctctgcaa	180
agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat	240
gtaggccagg gtgcgggataa tagtactatt gaactgactc agaattggtt cagaaataat	300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt	360
aataacgcgc cgctgggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt	420
ggttttggca acaacgccac ggctaaccag tattaa	456

<210> 2

<211> 456

<212> DNA

<213> Salmonella enteritidis

<400> 2

atgaaaaaca aattgttatt tatgatgttg acaatactgg gtgcgcctgg gattgcaacc	60
gcgcacaaatt atgatctggc tcgttcagaa tataattttg cggtaaatga attaagcaag	120
tcttcattta atcaggcggc cattatttgt caagtcggca cggtataatag tgccagagta	180
cgccaggaag gatcaaaact attgtccgtt atttcacaag aaggaggaaa taatcgggcy	240
aaagtcgacc aggcaggga ttataacttt gcgtatattg agcaaacggg caatgccaac	300
gatgccagta tatcgaaaag cgcttacggt aatagtgcag ctattatcca gaaaggttct	360
ggaaataagg ccaatattac ccagtacggt acgcagaaaa cagcagttgt agtgcagaaa	420
cagtcgcata tggctattcg cgtcacccaa cgctaa	456

<210> 3

<211> 456
 <212> DNA
 <213> E. Coli

<400> 3
 atgaaacttt taaaagtaga agcaattgca gcaatcgat tctccggtag cgctctggca 60
 ggtgttggtc ctacgtacgg cggcggcggg aaccacgggt gtggcggtaa taatagcggc 120
 ccaaattctg agctgaacat ttaccagtac ggtggcggtg actctgcact tgctctgcaa 180
 actgatgccc gtaactctga cttgactatt acccagcatg gcggcggtaa tggcgcagat 240
 gttggcagcagg gctcagatga cagctcaatc gatctgaccc aacgtggctt cggtaacagc 300
 gctactcttg atcagtgga cggcaaaaaat tctgaaatga cgggttaaaca gttcgggtgt 360
 ggcaacgggtg ctgcagttga ccagactgca tctaactcct ccgtcaacgt gactcaggtt 420
 ggctttggta acaacgcgac cgctcatcag tactaa 456

<210> 4
 <211> 456
 <212> DNA
 <213> E. Coli

<400> 4
 atgaaaaaca aattgttatt tatgatgtta acaatactgg gtgcgcctgg gattgcagcc 60
 gcagcagggt atgatttagc taattcagaa tataacttcg cggtaaatga attgagtaag 120
 tcttcattta atcaggcagc cataattggt caagctggga ctaataatag tgctcagtta 180
 cggcaggagg gctcaaaact tttggcgggt gttgcgcaag aaggtagtag caaccgggca 240
 aagattgacc agacaggaga ttataacctt gcataatatt atcaggcggg cagtgcacac 300
 gatgccagta tttcgcaagg tgcttatggt aatactgcga tgattatcca gaaagggttct 360
 ggtaataaag caaatattac acagtatggt actcaaaaaa cggcaattgt agtgcagaga 420
 cagtcgcaaa tggctatttc cgtgacacaa cggttaa 456

<210> 5
 <211> 151
 <212> PRT
 <213> Salmonella enteritidis

<400> 5
 Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1 5 10 15
 Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
 20 25 30
 Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
 35 40 45
 Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
 50 55 60
 Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
 65 70 75 80
 Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
 85 90 95
 Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
 100 105 110
 Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
 115 120 125
 Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
 130 135 140
 Asn Ala Thr Ala Asn Gln Tyr

145

150

<210> 6

<211> 151

<212> PRT

<213> *Salmonella enteritidis*

<400> 6

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Met Lys Asn Lys Leu Leu Phe Met Met Leu Thr Ile Leu Gly Ala Pro
 1           5           10           15
Gly Ile Ala Thr Ala Thr Asn Tyr Asp Leu Ala Arg Ser Glu Tyr Asn
          20          25          30
Phe Ala Val Asn Glu Leu Ser Lys Ser Ser Phe Asn Gln Ala Ala Ile
          35          40          45
Ile Gly Gln Val Gly Thr Asp Asn Ser Ala Arg Val Arg Gln Glu Gly
          50          55          60
Ser Lys Leu Leu Ser Val Ile Ser Gln Glu Gly Gly Asn Asn Arg Ala
65          70          75          80
Lys Val Asp Gln Ala Gly Asn Tyr Asn Phe Ala Tyr Ile Glu Gln Thr
          85          90          95
Gly Asn Ala Asn Asp Ala Ser Ile Ser Gln Ser Ala Tyr Gly Asn Ser
          100         105         110
Ala Ala Ile Ile Gln Lys Gly Ser Gly Asn Lys Ala Asn Ile Thr Gln
          115         120         125
Tyr Gly Thr Gln Lys Thr Ala Val Val Val Gln Lys Gln Ser His Met
          130         135         140
Ala Ile Arg Val Thr Gln Arg
145          150

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<210> 7

<211> 151

<212> PRT

<213> *Escherichia coli*

<400> 7

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Met Lys Leu Leu Lys Val Ala Ala Ile Ala Ala Ile Val Phe Ser Gly
 1           5           10           15
Ser Ala Leu Ala Gly Val Val Pro Gln Tyr Gly Gly Gly Gly Asn His
          20          25          30
Gly Gly Gly Gly Asn Asn Ser Gly Pro Asn Ser Glu Leu Asn Ile Tyr
          35          40          45
Gln Tyr Gly Gly Gly Asn Ser Ala Leu Ala Leu Gln Thr Asp Ala Arg
          50          55          60
Asn Ser Asp Leu Thr Ile Thr Gln His Gly Gly Gly Asn Gly Ala Asp
65          70          75          80
Val Gly Gln Gly Ser Asp Asp Ser Ser Ile Asp Leu Thr Gln Arg Gly
          85          90          95
Phe Gly Asn Ser Ala Thr Leu Asp Gln Trp Asn Gly Lys Asn Ser Glu
          100         105         110
Met Thr Val Lys Gln Phe Gly Gly Asn Gly Ala Ala Val Asp Gln
          115         120         125
Thr Ala Ser Asn Ser Ser Val Asn Val Thr Gln Val Gly Phe Gly Asn
          130         135         140
Asn Ala Thr Ala His Gln Tyr

```

145 150

<210> 8
 <211> 151
 <212> PRT
 <213> Escherichia coli

<400> 8
 Met Lys Asn Lys Leu Leu Phe Met Met Leu Thr Ile Leu Gly Ala Pro
 1 5 10 15
 Gly Ile Ala Ala Ala Ala Gly Tyr Asp Leu Ala Asn Ser Glu Tyr Asn
 20 25 30
 Phe Ala Val Asn Glu Leu Ser Lys Ser Ser Phe Asn Gln Ala Ala Ile
 35 40 45
 Ile Gly Gln Ala Gly Thr Asn Asn Ser Ala Gln Leu Arg Gln Gly Gly
 50 55 60
 Ser Lys Leu Leu Ala Val Val Ala Gln Glu Gly Ser Ser Asn Arg Ala
 65 70 75 80
 Lys Ile Asp Gln Thr Gly Asp Tyr Asn Leu Ala Tyr Ile Asp Gln Ala
 85 90 95
 Gly Ser Ala Asn Asp Ala Ser Ile Ser Gln Gly Ala Tyr Gly Asn Thr
 100 105 110
 Ala Met Ile Ile Gln Lys Gly Ser Gly Asn Lys Ala Asn Ile Thr Gln
 115 120 125
 Tyr Gly Thr Gln Lys Thr Ala Ile Val Val Gln Arg Gln Ser Gln Met
 130 135 140
 Ala Ile Arg Val Thr Gln Arg
 145 150

<210> 9
 <211> 48
 <212> DNA
 <213> Leishmania major

<400> 9
 tatgatcagc tgggtaccgc tggtgttacc catgaaatgg cacatgca

48

<210> 10
 <211> 16
 <212> PRT
 <213> Leishmania major

<400> 10
 Tyr Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala
 1 5 10 15

<210> 11
 <211> 456
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant Salmonella enteritidis 3b afgA
 sequence containing the replacement fragment

encoding PT3 from GP63 of *Leishmania major*.

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<400> 11
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct    60
ggcgtcgttc cacaatgggg cggcgggcgg aatcataacg gcggcgggcaa tagttccggc    120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa    180
agcgatgccc gtaaattctga aacgaccatt acccagagcg gttatggtaa cggcgccgat    240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat    300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt    360
aataacgccg cgctgggttaa ttatgatcag ctggttaccc gtgttggttac ccatgaaatg    420
gcacatgcaa acaacgccac ggctaaccag tattaa                                456
```

```
<210> 12
<211> 151
<212> PRT
<213> Artificial Sequence
```

```
<220>
<223> Recombinant Salmonella enteritidis 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of Leishmania major.
```

```
<400> 12
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1          5          10          15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
          20          25          30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
          35          40          45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
          50          55          60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65          70          75          80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
          85          90          95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
          100          105          110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Tyr
          115          120          125
Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala Asn
          130          135          140
Asn Ala Thr Ala Asn Gln Tyr
145          150
```

```
<210> 13
<211> 456
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Recombinant Salmonella enteritidis 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of Leishmania major.
```

```

<400> 13
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgtcgttc cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc      120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa      180
agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atatgatcag      360
ctggttaccc gtgttggttac ccatgaaatg gcacatgcaa gcgtaatggt gcgtcagggt      420
ggttttggca acaacgccac ggctaaccag tattaa                                456

```

```

<210> 14
<211> 151
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Recombinant Salmonella enteritidis 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of Leishmania major.

```

```

<400> 14
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1             5             10             15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
      20             25             30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35             40             45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
      50             55             60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65             70             75             80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
      85             90             95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
      100            105            110
Ile Thr Val Gly Gln Tyr Asp Gln Leu Val Thr Arg Val Val Thr His
      115            120            125
Glu Met Ala His Ala Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130            135            140
Asn Ala Thr Ala Asn Gln Tyr
145                150

```

```

<210> 15
<211> 456
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Recombinant Salmonella enteritidis 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of Leishmania major.

```

```

<400> 15
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60

```

```

ggcgtctatg atcagctggt taccogtggt gttacccatg aaatggcaca tgcacccggc 120
ccggactcaa cgttgagcat ttatcagtag gggtccgcta acgctgcgct tgctctgcaa 180
agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat 240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatgggtt cagaaataat 300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt 360
aataacgccc cgctgggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcaggtt 420
ggttttggca acaacgccac ggctaaccag tattaa 456

```

<210> 16
 <211> 151
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant *Salmonella enteritidis* 3b afgA
 sequence containing the replacement fragment
 encoding PT3 from GP63 of *Leishmania major*.

```

<400> 16
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1           5           10          15
Ser Ala Leu Ala Gly Val Tyr Asp Gln Leu Val Thr Arg Val Val Thr
      20          25          30
His Glu Met Ala His Ala Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35          40          45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
      50          55          60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65          70          75          80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
      85          90          95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
      100         105         110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
      115         120         125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130         135         140
Asn Ala Thr Ala Asn Gln Tyr
145          150

```

<210> 17
 <211> 456
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant *Salmonella enteritidis* 3b afgA
 sequence containing the replacement fragment
 encoding PT3 from GP63 of *Leishmania major*.

```

<400> 17
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct 60
ggcgtcggtt cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc 120
ccggactatg atcagctggt taccogtggt gttacccatg aaatggcaca tgcaactgcaa 180

```

```

agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt      360
aataacgccg cgctgggtaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt      420
ggttttggca acaacgccac ggctaaccag tattaa                                456

```

<210> 18
 <211> 151
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant Salmonella enteritidis 3b afgA
 sequence containing the replacement fragment
 encoding PT3 from GP63 of Leishmania major.

```

<400> 18
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1             5             10             15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
      20             25             30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Tyr Asp Gln Leu Val Thr
 35             40             45
Arg Val Val Thr His Glu Met Ala His Ala Leu Gln Ser Asp Ala Arg
 50             55             60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
 65             70             75             80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
      85             90             95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
      100            105            110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
      115            120            125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130            135            140
Asn Ala Thr Ala Asn Gln Tyr
145                        150

```

<210> 19
 <211> 456
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant Salmonella enteritidis 3b afgA
 sequence containing the replacement fragment
 encoding PT3 from GP63 of Leishmania major.

```

<400> 19
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgctcgtt cacaatgggg cggcggcggt aatcataacg gcggcggcaa tagttccggc      120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa      180
agcgatgccc gtaaatatga tcagctgggt acccggtgtt ttacccatga aatggcacat      240
gcaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300

```

```

gccaccatcg accagtggaa cgctaaaaaac tccgatatta ctgtcggcca atacggcggt 360
aataacgccg cgctgggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt 420
ggttttggca acaacgccac ggctaaccag tattaa 456

```

<210> 20
 <211> 151
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Recombinant *Salmonella enteritidis* 3b afgA
 sequence containing the replacement fragment
 encoding PT3 from GP63 of *Leishmania major*.

```

<400> 20
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1          5          10          15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
          20          25          30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
          35          40          45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
          50          55          60
Lys Tyr Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His
65          70          75          80
Ala Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
          85          90          95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
          100          105          110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
          115          120          125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
          130          135          140
Asn Ala Thr Ala Asn Gln Tyr
145          150

```

<210> 21
 <211> 456
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Recombinant *Salmonella enteritidis* 3b afgA
 sequence containing the replacement fragment
 encoding PT3 from GP63 of *Leishmania major*.

```

<400> 21
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct 60
ggcgtcgttc cacaatgggg cggcggcggt aatcataacg gcggcgcaa tagttccggc 120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa 180
agcgatgccc gtaaatctga aacgaccatt acccagagcg gttatggtaa cggcgccgat 240
gtaggccagg gtgcggataa ttatgatcag ctggttaccc gtgttggtac ccatgaaatg 300
gcacatgcag accagtggaa cgctaaaaaac tccgatatta ctgtcggcca atacggcggt 360
aataacgccg cgctgggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt 420

```

ggttttggca acaacgccac ggctaaccag tattaa

456

<210> 22

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of *Leishmania major*.

<400> 22

```

Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1           5           10           15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
 20           25           30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
 35           40           45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
 50           55           60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
 65           70           75           80
Val Gly Gln Gly Ala Asp Asn Tyr Asp Gln Leu Val Thr Arg Val Val
 85           90           95
Thr His Glu Met Ala His Ala Asp Gln Trp Asn Ala Lys Asn Ser Asp
100          105          110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
115          120          125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
130          135          140
Asn Ala Thr Ala Asn Gln Tyr
145          150

```

<210> 23

<211> 456

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of *Leishmania major*.

<400> 23

```

atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgtcgttc cacaatgggg cggcggcggt aatcataacg gcggcggcga tagttccggc      120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa      180
agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
gccaccatcg accagtggaa cgctaaaaac tatgatcagc tggttaccgg tgttgttacc      360
catgaaatgg cacatgcaaa tcagaccgca tctgattcca gcgtaatggg gcgtcaggtt      420
ggttttggca acaacgccac ggctaaccag tattaa                                456

```

<210> 24
 <211> 151
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA
 sequence containing the replacement fragment
 encoding PT3 from GP63 of *Leishmania major*.

<400> 24

```

Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
1      5      10      15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
20      25      30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
35      40      45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
50      55      60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65      70      75      80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
85      90      95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Tyr Asp
100     105     110
Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala Asn Gln
115     120     125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
130     135     140
Asn Ala Thr Ala Asn Gln Tyr
145     150

```

<210> 25
 <211> 456
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA
 sequence containing the replacement fragment
 encoding PT3 from GP63 of *Leishmania major*.

<400> 25

```

atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgctcggtt cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc      120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct ttatgatcag      180
ctggttaccc gtgttggttac ccatgaaatg gcacatgcag gttatggtaa cggcgccgat      240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt      360
aataacgccg cgctgggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt      420
ggttttggca acaacgccac ggctaaccag tattaa      456

```

<210> 26
 <211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of *Leishmania major*.

<400> 26

```

Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1           5           10           15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
      20           25           30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35           40           45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Tyr Asp Gln Leu Val Thr Arg
      50           55           60
Val Val Thr His Glu Met Ala His Ala Gly Tyr Gly Asn Gly Ala Asp
65           70           75           80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
      85           90           95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
      100          105          110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
      115          120          125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130          135          140
Asn Ala Thr Ala Asn Gln Tyr
145          150

```

<210> 27

<211> 456

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of *Leishmania major*.

<400> 27

```

atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgtcggtc cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc      120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa      180
agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
tatgatcagc tggttacccg tgttgttacc catgaaatgg cacatgcatt cagaaataat      300
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt      360
aataacgccg cgctgggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt      420
ggttttgcca acaacgccac ggctaaccag tattaa      456

```

<210> 28

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of *Leishmania major*.

<400> 28

```

Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1           5           10           15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
          20           25           30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
          35           40           45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
          50           55           60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65           70           75           80
Tyr Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala
          85           90           95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
          100          105          110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
          115          120          125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
          130          135          140
Asn Ala Thr Ala Asn Gln Tyr
145           150

```

<210> 29

<211> 456

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of *Leishmania major*.

<400> 29

```

atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgtcggtc cacaatgggg cggcggcggt aatcataacg gcggcgggcaa tagttccggc      120
ccggactcaa cgttgagcat ttatcagtac ggttccgcta acgctgcgct tgctctgcaa      180
agcgatgccc gtaaactctga aacgaccatt acccagagcg gttatggtaa cggcgccgat      240
gtaggccagg gtgcgggataa tagtactatt gaactgactc agaatggttt cagaaataat      300
gccacctatg atcagctggg taccocgtgtt gttacccatg aaatggcaca tgcaggcggt      360
aataacgccg cgctgggttaa tcagaccgca tctgattcca gcgtaatggg gcgtcagggt      420
ggttttggca acaacgccac ggctaaccag tattaa                                456

```

<210> 30

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA
sequence containing the replacement fragment
encoding PT3 from GP63 of *Leishmania major*.

<400> 30

```

Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
 1           5           10           15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His
          20           25           30
Asn Gly Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35           40           45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
 50           55           60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65           70           75           80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
          85           90           95
Phe Arg Asn Asn Ala Thr Tyr Asp Gln Leu Val Thr Arg Val Val Thr
          100          105          110
His Glu Met Ala His Ala Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
      115          120          125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
 130          135          140
Asn Ala Thr Ala Asn Gln Tyr
145          150

```

<210> 31

<211> 131

<212> PRT

<213> *Salmonella enteritidis*

<400> 31

```

Gly Val Val Pro Gln Trp Gly Gly Gly Gly Asn His Asn Gly Gly Gly
 1           5           10           15
Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr Gln Tyr Gly Ser
          20           25           30
Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg Lys Ser Glu Thr
      35           40           45
Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp Val Gly Gln Gly
 50           55           60
Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly Phe Arg Asn Asn
65           70           75           80
Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp Ile Thr Val Gly
          85           90           95
Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln Thr Ala Ser Asp
      100          105          110
Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn Asn Ala Thr Ala
      115          120          125
Asn Gln Tyr
130

```

<210> 32

<211> 70

<212> PRT

<213> Salmonella enteritidis

<400> 32

```

Ala Arg Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly
 1           5           10           15
Ala Asp Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln
          20           25           30
Asn Gly Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Lys Asn Asp
          35           40           45
Ile Val Gly Tyr Gly Asn Ala Leu Asn Thr Ser Asp Ser Val Met Val
          50           55           60
Arg Val Gly Ala Asn Tyr
65           70

```

<210> 33

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence of the five internal repeats of AgfA.

<221> VARIANT

<222> (1)...(23)

<223> Xaa = Any Amino Acid

<400> 33

```

Ser Xaa Xaa Xaa Xaa Xaa Gln Xaa Gly Xaa Xaa Asn Xaa Ala Xaa Xaa
 1           5           10           15
Xaa Gln Xaa Xaa Ala Xaa Xaa
          20

```

<210> 34

<211> 109

<212> PRT

<213> Salmonella enteritidis

<400> 34

```

Ser Thr Leu Ser Ile Tyr Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala
 1           5           10           15
Leu Gln Ser Asp Ala Arg Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly
          20           25           30
Tyr Gly Asn Gly Ala Asp Val Gly Gln Gly Ala Asp Asn Ser Thr Ile
          35           40           45
Glu Leu Thr Gln Asn Gly Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp
          50           55           60
Asn Ala Lys Asn Ser Asp Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn
65           70           75           80
Ala Ala Leu Val Asn Gln Thr Ala Ser Asp Ser Ser Val Met Val Arg
          85           90           95
Gln Val Gly Phe Gly Asn Asn Ala Thr Ala Asn Gln Tyr
          100          105

```

<210> 35
 <211> 109
 <212> PRT
 <213> *Escherichia coli*

<400> 35
 Ser Glu Leu Asn Ile Tyr Gln Tyr Gly Gly Gly Asn Ser Ala Leu Ala
 1 5 10 15
 Leu Gln Thr Asp Ala Arg Asn Ser Asp Leu Thr Ile Thr Gln His Gly
 20 25 30
 Gly Gly Asn Gly Ala Asp Val Gly Gln Gly Ser Asp Asp Ser Ser Ile
 35 40 45
 Asp Leu Thr Gln Arg Gly Phe Gly Asn Ser Ala Thr Leu Asp Gln Trp
 50 55 60
 Asn Gly Lys Asn Ser Glu Met Thr Val Lys Gln Phe Gly Gly Gly Asn
 65 70 75 80
 Gly Ala Ala Val Asp Gln Thr Ala Ser Asn Ser Ser Val Asn Val Thr
 85 90 95
 Gln Val Gly Phe Gly Asn Asn Ala Thr Ala His Gln Tyr
 100 105

<210> 36
 <211> 56
 <212> PRT
 <213> *Serratia marcescens*

<400> 36
 Ile Glu Asn Ala Ile Gly Gly Ser Gly Asn Asp Val Ile Val Gly Asn
 1 5 10 15
 Ala Ala Asn Asn Val Leu Lys Gly Gly Ala Gly Asn Asp Val Leu Phe
 20 25 30
 Gly Gly Gly Gly Ala Asp Glu Leu Trp Gly Gly Ala Gly Lys Asp Ile
 35 40 45
 Phe Val Phe Ser Ala Ala Ser Asp
 50 55

<210> 37
 <211> 68
 <212> PRT
 <213> *Salmonella enteritidis*

<400> 37
 Ser Thr Leu Ser Ile Tyr Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala
 1 5 10 15
 Leu Gln Ser Asp Ala Arg Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly
 20 25 30
 Tyr Gly Asn Gly Ala Asp Val Gly Gln Gly Ala Asp Asn Ser Thr Ile
 35 40 45
 Glu Leu Thr Gln Asn Gly Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp
 50 55 60
 Asn Ala Lys Asn
 65

<210> 38

<211> 47
 <212> PRT
 <213> bovine

<400> 38
 Val Ile Ile Ser Lys Lys Gly Asp Ile Ile Thr Ile Arg Thr Glu Ser
 1 5 10 15
 Pro Phe Lys Asn Thr Glu Ile Ser Phe Lys Leu Gly Gln Glu Phe Glu
 20 25 30
 Glu Thr Thr Ala Asp Asn Arg Lys Thr Lys Ser Thr Val Thr Leu
 35 40 45

<210> 39
 <211> 48
 <212> PRT
 <213> Salmonella enteritidis

<400> 39
 Leu Ser Ile Tyr Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln
 1 5 10 15
 Ser Asp Ala Arg Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly
 20 25 30
 Asn Gly Ala Asp Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu
 35 40 45

<210> 40
 <211> 19
 <212> PRT
 <213> Unknown

<220>
 <223> Beta-prism motif of the vitelline membrane outer
 layer protein I (VMO-I)

<400> 40
 Phe Ala Leu Lys Val Glu Pro Ser Gln Phe Gly Arg Asp Asp Thr Ala
 1 5 10 15
 Leu Asn Gly

<210> 41
 <211> 19
 <212> PRT
 <213> Unknown

<220>
 <223> Beta-prism motif of the vitelline membrane outer
 layer protein I (VMO-I)

<400> 41
 Phe Ser Leu Arg Ser Glu Lys Ser Gln Gly Gly Gly Asp Asp Thr Ala
 1 5 10 15
 Ala Asn Asn

<210> 42
 <211> 19
 <212> PRT
 <213> Unknown

<220>
 <223> Beta-prism motif of the vitelline membrane outer
 layer protein I (VMO-I)

<400> 42
 Leu Gln Thr Lys Val Glu Ser Pro Gln Gly Leu Arg Asp Asp Thr Ala
 1 5 10 15
 Leu Asn Asn

<210> 43
 <211> 16
 <212> PRT
 <213> Unknown

<220>
 <223> Beta-prism motif of the vitelline membrane outer
 layer protein I (VMO-I)

<400> 43
 Leu Ser Ile Tyr Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln
 1 5 10 15

<210> 44
 <211> 16
 <212> PRT
 <213> Unknown

<220>
 <223> Beta-prism motif of the vitelline membrane outer
 layer protein I (VMO-I)

<400> 44
 Ile Glu Leu Thr Gln Asn Gly Phe Arg Asn Asn Ala Thr Ile Asp Gln
 1 5 10 15

<210> 45
 <211> 16
 <212> PRT
 <213> Unknown

<220>
 <223> Beta-prism motif of the vitelline membrane outer
 layer protein I (VMO-I)

<400> 45
 Val Met Val Arg Gln Val Gly Phe Gly Asn Asn Ala Thr Ala Asn Gln
 1 5 10 15

<210> 46
 <211> 143
 <212> PRT
 <213> *Salmonella enteritidis*

<400> 46
 Ala Gly Phe Val Gly Asn Lys Ala Val Val Gln Ala Ala Val Thr Ile
 1 5 10 15
 Ala Ala Gln Asn Thr Thr Ser Ala Asn Trp Ser Gln Asp Pro Gly Phe
 20 25 30
 Thr Gly Pro Ala Val Ala Ala Gly Gln Lys Val Gly Thr Leu Ser Ile
 35 40 45
 Thr Ala Thr Gly Pro His Asn Ser Val Ser Ile Ala Gly Lys Gly Ala
 50 55 60
 Ser Val Ser Gly Gly Val Ala Thr Val Pro Phe Val Asp Gly Gln Gly
 65 70 75 80
 Gln Pro Val Phe Arg Gly Arg Ile Gln Gly Ala Asn Ile Asn Asp Gln
 85 90 95
 Ala Asn Thr Gly Ile Asp Gly Leu Ala Gly Trp Arg Val Ala Ser Ser
 100 105 110
 Gln Glu Thr Leu Asn Val Pro Val Thr Thr Phe Gly Lys Ser Thr Leu
 115 120 125
 Pro Ala Gly Phe Thr Ala Thr Phe Tyr Val Gln Gln Tyr Gln Asn
 130 135 140

<210> 47
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 47
 ttggaattct tcttaaattt ttaaaatggc gttgagtat

39

<210> 48
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer

<400> 48
 agcatgagcc atttcatgtg taacaacacg tgtaacgagc tgatcatatg caatagtaac
 cgctgcctga accactgc

60

78

<210> 49
 <211> 78
 <212> DNA
 <213> Artificial Sequence

<220>

<223> PCR primer

<400> 49

tatgatcagc tctgttacacg tgttggttaca catgaaatgg ctcatgctgg gcctgctggt 60
gctgctggtc agaaagtt 78

<210> 50

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 50

attaagctta tacataatcc ctctttaagt ttttgcattg 39

<210> 51

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 51

gcagaattca gcagttgtag tgcagaaaca gtcgcatat 39

<210> 52

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 52

tgcattgtgcc atttcatggg taacaacacg ggtaaccagc tgatcatagt ttttagcgtt 60
ccactggtcg atggtggc 78

<210> 53

<211> 78

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 53

tatgatcagc tggttaccgc tgttggttacc catgaaatgg cacatgcaaa tcagaccgca 60
tctgattcca gcgtaatg 78

<210> 54

<211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 54
 agacgcaagc ttcgtttaat gtgacctgag ggatcaccg 39

 <210> 55
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 55
 gggatgttgt gtaaagataa aaaaatagtg 30

 <210> 56
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 56
 tgcccaatct taggccataa tatttttgtg 30

 <210> 57
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 57
 aggaaggatc aaaactattg tccgttatTTT cac 33

 <210> 58
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer

 <400> 58
 tatatttaca ctaagacgag acaactcaat cgg 33

<210> 59
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence

<221> VARIANT
<222> (1)...(18)
<223> Xaa = Any Amino Acid

<400> 59
Ser Xaa Xaa Xaa Xaa Xaa Gln Xaa Gly Xaa Xaa Asn Xaa Ala Xaa Xaa
1 5 10 15
Xaa Gln